



## SEQUENCE LISTING

<110> Hayward, Nicholas K.  
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Grimmond, Sean  
Nordenskjold, Magnus  
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
SAME

<130> Dav. Col. Cave

<140> 09/349,954  
<141> 1999-07-08

<150> 08/765,588  
<151> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

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<212> DNA  
<213> Nucleotide Sequence of VEGF165

<220>  
<221> CDS  
<222> (17)..(589)

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gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100  
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro  
15 20 25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148  
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met  
30 35 40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196  
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp  
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atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

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Cys	Val	Pro	Leu	Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu		
			80					85					90				
gag	tgt	gtg	ccc	act	gag	gag	tcc	aac	atc	acc	atg	cag	att	atg	cgg	340	
Glu	Cys	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg		
		95					100					105					
atc	aaa	cct	cac	caa	ggc	cag	cac	ata	gga	gag	atg	agc	ttc	cta	cag	388	
Ile	Lys	Pro	His	Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln		
	110					115					120						
cac	aac	aaa	tgt	gaa	tgc	aga	cca	aag	aaa	gat	aga	gca	aga	caa	gaa	436	
His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu		
125					130					135					140		
aat	ccc	tgt	ggg	cct	tgc	tca	gag	cgg	aga	aag	cat	ttg	ttt	gta	caa	484	
Asn	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu	Phe	Val	Gln		
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gat	ccg	cag	acg	tgt	aaa	tgt	tcc	tgc	aaa	aac	aca	gac	tcg	cgt	tgc	532	
Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys		
			160					165					170				
aag	gcg	agg	cag	ctt	gag	tta	aac	gaa	cgt	act	tgc	aga	tgt	gac	aag	580	
Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg	Cys	Asp	Lys		
		175					180					185					
ccg	agg	cgg	tgagccgggc	aggaggaagg	agcctccctc	agcggtttcgg										629	
Pro	Arg	Arg															
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gaaccagatc	tctcaccagg															649	

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 <213> Nucleotide Sequence of VEGF165

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 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
                     35                    40                    45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
           50                    55                    60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
   65                    70                    75                    80  
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
                     85                    90                    95  
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
                     100                    105                    110  
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
                     115                    120                    125  
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly  
   130                    135                    140  
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
 145                    150                    155                    160  
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln  
                     165                    170                    175  
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg  
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 <213> Nucleotide Sequence of SOM175

<220>  
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 <222> (3)..(623)

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 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                     20                    25                    30

cag	agg	aaa	gtg	gtg	tca	tgg	ata	gat	gtg	tat	act	cgc	gct	acc	tgc	143
Gln	Arg	Lys	Val <sub>35</sub>	Val	Ser	Trp	Ile	Asp <sub>40</sub>	Val	Tyr	Thr	Arg	Ala <sub>45</sub>	Thr	Cys	
cag	ccc	cgg	gag	gtg	gtg	gtg	ccc	ttg	act	gtg	gag	ctc	atg	ggc	acc	191
Gln	Pro	Arg <sub>50</sub>	Glu	Val	Val	Val	Pro <sub>55</sub>	Leu	Thr	Val	Glu	Leu <sub>60</sub>	Met	Gly	Thr	
gtg	gcc	aaa	cag	ctg	gtg	ccc	agc	tgc	gtg	act	gtg	cag	cgc	tgt	ggt	239
Val	Ala <sub>65</sub>	Lys	Gln	Leu	Val	Pro <sub>70</sub>	Ser	Cys	Val	Thr	Val <sub>75</sub>	Gln	Arg	Cys	Gly	
ggc	tgc	tgc	cct	gac	gat	ggc	ctg	gag	tgt	gtg	ccc	act	ggg	cag	cac	287
Gly <sub>80</sub>	Cys	Cys	Pro	Asp	Asp <sub>85</sub>	Gly	Leu	Glu	Cys	Val <sub>90</sub>	Pro	Thr	Gly	Gln	His <sub>95</sub>	
caa	gtc	cgg	atg	cag	atc	ctc	atg	atc	cgg	tac	ccg	agc	agt	cag	ctg	335
Gln	Val	Arg	Met	Gln <sub>100</sub>	Ile	Leu	Met	Ile	Arg <sub>105</sub>	Tyr	Pro	Ser	Ser	Gln <sub>110</sub>	Leu	
ggg	gag	atg	tcc	ctg	gaa	gaa	cac	agc	cag	tgt	gaa	tgc	aga	cct	aaa	383
Gly	Glu	Met	Ser <sub>115</sub>	Leu	Glu	Glu	His	Ser <sub>120</sub>	Gln	Cys	Glu	Cys	Arg <sub>125</sub>	Pro	Lys	
aaa	aag	gac	agt	gct	gtg	aag	cca	gac	agg	gct	gcc	act	ccc	cac	cac	431
Lys	Lys	Asp <sub>130</sub>	Ser	Ala	Val	Lys	Pro <sub>135</sub>	Asp	Arg	Ala	Ala	Thr <sub>140</sub>	Pro	His	His	
cgt	ccc	cag	ccc	cgt	tct	gtt	ccg	ggc	tgg	gac	tct	gcc	ccc	gga	gca	479
Arg	Pro <sub>145</sub>	Gln	Pro	Arg	Ser	Val <sub>150</sub>	Pro	Gly	Trp	Asp	Ser <sub>155</sub>	Ala	Pro	Gly	Ala	
ccc	tcc	cca	gct	gac	atc	acc	cat	ccc	act	cca	gcc	cca	ggc	ccc	tct	527
Pro <sub>160</sub>	Ser	Pro	Ala	Asp	Ile <sub>165</sub>	Thr	His	Pro	Thr	Pro <sub>170</sub>	Ala	Pro	Gly	Pro <sub>175</sub>	Ser	
gcc	cac	gct	gca	ccc	agc	acc	acc	agc	gcc	ctg	acc	ccc	gga	cct	gcc	575
Ala	His	Ala	Ala	Pro <sub>180</sub>	Ser	Thr	Thr	Ser	Ala <sub>185</sub>	Leu	Thr	Pro	Gly	Pro <sub>190</sub>	Ala	
gct	gcc	gct	gcc	gac	gcc	gca	gct	tcc	tcc	gtt	gcc	aag	ggc	ggg	gct	623
Ala	Ala	Ala	Ala <sub>195</sub>	Asp	Ala	Ala	Ala	Ser <sub>200</sub>	Ser	Val	Ala	Lys	Gly <sub>205</sub>	Gly	Ala	

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 agactcagca gggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743  
 tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803  
 ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863  
 agagtgggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923  
 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattttaca actggctctt 983  
 cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tggtaacaaga 1043  
 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

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 <213> Nucleotide Sequence of SOM175

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 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg

130		135		140
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro				
145		150		155
Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala				
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His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala				
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Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala				
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<210> 5  
 <211> 993  
 <212> DNA  
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<220>  
 <221> CDS  
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 1 5 10 15  
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
 20 25 30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
 35 40 45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
 50 55 60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
 65 70 75  
 ggc tgc tgc cct gac gat gcc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
 80 85 90 95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335  
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
 100 105 110  
 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383  
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
 115 120 125  
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431  
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro  
 130 135 140  
 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479  
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys  
 145 150 155  
 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527  
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu  
 160 165 170 175  
 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576  
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
 180 185  
 cttttcagac tcagcagggt gacttgcttc agaggctata tcccagtgagg ggaacaaagg 636  
 ggagcctggt aaaaaacagc caagcccca agacctcagc ccaggcagaa gctgctctag 696  
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 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876  
 gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt gggctttggt 936  
 acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993

<210> 6  
 <211> 188  
 <212> PRT  
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6  
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
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Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45  
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60  
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80  
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95  
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
100 105 110  
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
115 120 125  
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg  
130 135 140  
Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg  
145 150 155 160  
Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu  
165 170 175  
Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
180 185

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<222> (3)..(431)

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ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95



Leu	Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His		
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cag	agg	aaa	gtg	gtg	tca	tgg	ata	gat	gtg	tat	act	cgc	gct	acc	tgc	143	
Gln	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys		
			35					40					45				
cag	ccc	cgg	gag	gtg	gtg	gtg	ccc	ttg	act	gtg	gag	ctc	atg	ggc	acc	191	
Gln	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr		
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gtg	gcc	aaa	cag	ctg	gtg	ccc	agc	tgc	gtg	act	gtg	cag	cgc	tgt	ggc	239	
Val	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly		
	65					70					75						
ggc	tgc	tgc	cct	gac	gat	ggc	ctg	gag	tgt	gtg	ccc	act	ggg	cag	cac	287	
Gly	Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His		
80				85						90					95		
caa	gtc	cgg	atg	cag	atc	ctc	atg	atc	cgg	tac	ccg	agc	agt	cag	ctg	335	
Gln	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu		
				100					105					110			
ggg	gag	atg	tcc	ctg	gaa	gaa	cac	agc	cag	tgt	gaa	tgc	aga	cct	aaa	383	
Gly	Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys		
			115					120					125				
aaa	aag	gac	agt	gct	gtg	aag	cca	gat	agg	tgc	cgg	aag	ctg	cga	agg	431	
Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Cys	Arg	Lys	Leu	Arg	Arg		
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ggaacaaagg	ggagcctggg	aaaaaacagc	caagccccc	agacctcagc	ccaggcagaa	551											
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catcatcaaa	caggacagag	ttggaagagg	agactgggag	gcagcaagag	gggtcacata	671											
ccagctcagg	ggagaatgga	gtactgtctc	agtttctaac	cactctgtgc	aagtaagcat	731											
cttacaactg	gctcttctc	ccctcactaa	gaagacccaa	acctctgcat	aatgggattt	791											

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aaaaaaaa

858

<210> 8

<211> 143

<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exons 6&7

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
130 135 140

<210> 9

<211> 910

<212> DNA

<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>

<221> CDS

<222> (3)..(305)

<400> 9

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1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
                     20                    25                    30  
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
                     35                    40                    45  
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
                     50                    55                    60  
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
                     65                    70                    75  
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
                     80                    85                    90                    95  
 caa gtc cgg atg cag acc taaaaaaaaag gacagtgtgtg tgaagccaga 335  
 Gln Val Arg Met Gln Thr  
                     100  
 cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395  
 ccccggagca ccctccccag ctgacatcac ccctcccaact ccagccccag gccctctctgc 455  
 ccacgttgca ccagcacca ccagcgccct gacccccgga cctgccgctg ccgctgccga 515  
 cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575  
 tgccggaagc tgcgaaggtg acacatggct tttcagactc agcagggtga cttgcctcag 635  
 aggctatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccacaaga 695  
 cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755  
 ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815  
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910

<210> 10

<211> 101

<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95

Val Arg Met Gln Thr  
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<210> 11

<211> 42

<212> DNA

<213> Oligonucleotide

<400> 11

accaccacct ccctgggctg gcatgtggca cgtgcataaa cg

42

<210> 12

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<213> Oligonucleotide

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agttgtttga ccacattgcc catgagttcc atgctcagag gc

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<210> 13

<211> 38

<212> DNA

<213> Oligonucleotide

<400> 13

gacacctgggg ctggagtggg atggatgatg tcagctgg 38

<210> 14

<211> 40

<212> DNA

<213> Oligonucleotide

<400> 14

gcgggcagag gacacctgggg ctgtctggcc tcacagcact 40

<210> 15

<211> 236

<212> DNA

<213> Human SOM175

<400> 15

atgagggggcc aggtacgtga ggtctccac agggccctgg aaagaatact tacatctgct 60  
cccatgggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120  
ttttcaagac ctaaagacag gtgagtcttt ctctccgta ggctgcctcc agccccaggc 180  
ccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16

<211> 1242

<212> DNA

<213> mVRF

<220>

<221> CDS

<222> (166)..(789)

<400> 16

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ggcggctctg gctgaccccc cccacaccg ccgggctagg gcccg atg agc ccc ctg 177  
Met Ser Pro Leu  
1  
ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu	Ala	Arg	Thr	Gln	
5					10					15					20	
gcc	cct	gtg	tcc	cag	ttt	gat	ggc	ccc	agt	cac	cag	aag	aaa	gtg	gtg	273
Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln	Lys	Lys	Val	Val	
				25					30					35		
cca	tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	ccc	agg	gag	gtg	321
Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln	Pro	Arg	Glu	Val	
			40					45					50			
gtg	gtg	cct	ctg	agc	atg	gaa	ctc	atg	ggc	aat	gtg	gtc	aaa	caa	cta	369
Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val	Val	Lys	Gln	Leu	
		55					60					65				
gtg	ccc	agc	tgt	gtg	act	gtg	cag	cgc	tgt	ggc	ggc	tgc	tgc	cct	gac	417
Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	Cys	Pro	Asp	
	70					75					80					
gat	ggc	ctg	gaa	tgt	gtg	ccc	act	ggg	caa	cac	caa	gtc	cga	atg	cag	465
Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	Arg	Met	Gln	
85					90					95					100	
atc	ctc	atg	atc	cag	tac	ccg	agc	agt	cag	ctg	ggg	gag	atg	tcc	ctg	513
Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	Met	Ser	Leu	
				105					110					115		
gga	gaa	cac	agc	caa	tgt	gaa	tgc	aga	cct	aaa	aaa	aag	gag	agt	gct	561
Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	Glu	Ser	Ala	
			120					125					130			
gtg	agg	cca	gac	agg	gtt	gcc	ata	ccc	cac	cac	cgt	ccc	cag	ccc	cgc	609
Val	Arg	Pro	Asp	Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	
		135					140					145				
tct	gtt	ccg	ggc	tgg	gac	tct	acc	ccg	gga	gca	ccc	tcc	cca	gct	gac	657
Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	
	150					155					160					
atc	atc	cat	ccc	act	cca	gcc	cca	gga	tcc	tct	gcc	cgc	ctt	gca	ccc	705
Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	
165					170					175					180	
agc	gcc	gcc	aac	gcc	ctg	acc	ccc	gga	cct	gcc	gtt	gcc	gct	gta	gac	753
Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val	Ala	Ala	Val	Asp	

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185              190              195
gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc      799
Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
200              205
agacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacgggc 859
ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacctcct 919
cagtctggga ggctactgcc ccaggacctg gaccttttag agagctctct cgccatcttt 979
tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctgaggggcc 1039
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ctcactatga aaaccccaaa cttctaccaa taacgggatt tgggttctgt tatgataact 1159
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<210> 17
<211> 207
<212> PRT
<213> mVRF

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Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
20      25      30
Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
35      40      45
Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
50      55      60
Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65      70      75      80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85      90      95
Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
100      105      110
Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115      120      125
Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
130      135      140

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Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro
145					150					155					160
Ser	Pro	Ala	Asp	Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala
				165					170					175	
Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val
			180					185					190		
Ala	Ala	Val	Asp	Ala	Ala	Ala	Ser	Ser	Ile	Ala	Lys	Gly	Gly	Ala	
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<210> 18  
 <211> 188  
 <212> PRT  
 <213> mVRF167

<400> 18															
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Ala	Arg	Thr	Gln	Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln
			20					25					30		
Lys	Lys	Val	Val	Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln
		35					40					45			
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val
	50					55					60				
Val	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly
65					70					75					80
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
				85					90					95	
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
			100					105					110		
Glu	Met	Ser	Leu	Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
		115					120					125			
Lys	Glu	Ser	Ala	Val	Arg	Pro	Asp	Ser	Pro	Arg	Ile	Leu	Cys	Pro	Pro
	130					135					140				
Cys	Thr	Gln	Arg	Arg	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg
145					150					155					160
Cys	Arg	Arg	Arg	Arg	Phe	Leu	His	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu
				165					170					175	
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Pro	Arg	Lys				
			180					185							

<210> 19  
 <211> 188



<212> PRT  
<213> hVRF167

<400> 19

Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	Leu		
1				5					10					15			
Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln		
			20					25					30				
Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln		
		35					40					45					
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val		
	50					55					60						
Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly		
65					70					75					80		
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln		
				85					90					95			
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly		
			100					105					110				
Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys		
		115					120					125					
Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro	Arg		
	130					135					140						
Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg		
145					150					155					160		
Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu		
				165					170					175			
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg						
			180					185									

<210> 20  
<211> 71  
<212> PRT  
<213> mVRF186

<400> 20

Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly		
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Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	Ile	Ile	His	Pro		
			20					25					30				
Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn		
		35					40					45					

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser  
 50 55 60

Ser Ile Ala Lys Gly Gly Ala  
 65 70

<210> 21  
 <211> 71  
 <212> PRT  
 <213> hVRF186

<400> 21  
 Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly  
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Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro  
 20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser  
 35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ala Ser  
 50 55 60

Ser Val Ala Lys Gly Gly Ala  
 65 70

<210> 22  
 <211> 214  
 <212> PRT  
 <213> mVEGF188

<400> 22  
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 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly  
 20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg  
 35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr  
 50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met  
 65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr  
 85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln  
 100 105 110

Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu  
115 120 125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg  
130 135 140

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys  
145 150 155 160

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu  
165 170 175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp  
180 185 190

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg  
195 200 205

Cys Asp Lys Pro Arg Arg  
210